IN THE CLAIMS:

Please note that all claims currently pending are provided in clean form below. A marked up-version of the claim amendments is provided herewith.

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1. (Amended five times) A pair of nucleic acid probes for detection of chromosomal aberrations in hematological malignancies and having comparable size, said size being selected from the group consisting of from 1 to 100 kb, from 1 to 10 kb, 7 to 15 kb, 10 to 20 kb, 10 to 30 kb, 20 to 40 kb, 30 to 50 kb, 40 to 60 kb, 50 to 70 kb, 60 to 80 kb, 70 to 90 kb, and 80 to 100 kb, and flanking a potential breakpoint in a single chromosome, each of said pair of probes being labeled with at least one different reporter molecule such that a split signal arises after a break within said potential breakpoint.

2. (Amended five times) A pair of nucleic acid probes for detection of chromosomal aberrations in hematological malignancies, said nucleic acid probes of comparable size, said size being selected from the group consisting of from 1 to 100 kb, from 1 to 10 kb, 7 to 15 kb, 10 to 20 kb, 10 to 30 kb, 20 to 40 kb, 30 to 50 kb, 40 to 60 kb, 50 to 70 kb, 60 to 80 kb, 70 to 90 kb, and 80 to 100 kb, and flanking a potential breakpoint in a single chromosome, which pair of nucleic acid probes hybridize to a nucleic acid molecule at a genomic distance of 50 kb to no more than 100 kb.

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3. (Amended four times) The pair of nucleic acid probes of comparable size of claim 1, which pair of nucleic acid probes hybridize to a nucleic acid molecule at a genomic distance of 50 kb to no more than 100 kb.

4. (Previously amended four times) The pair of nucleic acid probes of claim 2, each of said pair of nucleic acid probes being labeled directly or indirectly with at least one reporter molecule.

5. (Previously three times amended) The pair of nucleic acid probes of claim 4 wherein the at least one reporter molecule is selected from the group consisting of enzymes, chromophores, fluorochromes, and haptens.

6. (Previously amended four times) The pair of nucleic acid probes of claim 5 wherein the pair of nucleic acid probes hybridize to a single corresponding nucleic acid molecule.

7. (Previously three amended) The pair of nucleic acid probes of claim 6 wherein the single corresponding nucleic acid molecule is at least a fragment of a chromosome.

8. (Previously three amended) The pair of nucleic acid probes of claim 7 wherein the chromosome is not aberrant.

9. (Previously three times amended) The pair of nucleic acid probes of claim 1 which hybridize *in situ.*

Please cancel claim 10 without prejudice or disclaimer.

11. (Amended five times) A method of detecting a nucleic acid molecule having a chromosomal aberration, said method comprising:

providing a pair of nucleic acid probes to detect chromosomal aberrations in hematological malignancies and to analyze a sample believed to contain said nucleic acid, said pair of nucleic acid probes having comparable size, said size being selected from the group consisting of 1 to 100 kb, 1 to 10 kb, 7 to 15 kb, 10 to 20 kb, 10 to 30 kb, 20 to 40 kb, 30 to 50 kb, 40 to 60 kb, 50 to 70 kb, 60 to 80 kb, 70 to 90 kb and 80 to 100 kb, and said pair of nucleic acid probes flanking a potential breakpoint in a single chromosome, each of said pair of nucleic acid probes being labeled with at least one different reporter molecule;

hybridizing said pair of nucleic acid probes to said nucleic acid; and

detecting the presence of a split signal that arises after a break within said potential breakpoint in the case of a chromosomal aberration.

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12. (Amended twice) A method of detecting cells suspected of having a chromosomal aberration, said method comprising:

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providing a pair of nucleic acid probes to detect chromosomal aberrations in hematological malignancies and to analyze nucleic acid of said cells, said pair of nucleic acid probes having comparable size, said size being selected from the group consisting of 1 to 100 kb, 1 to 10 kb, 7 to 15 kb, 10 to 20 kb, 10 to 30 kb, 20 to 40 kb, 30 to 50 kb, 40 to 60 kb, 50 to 70 kb, 60 to 80 kb, 70 to 90 kb and 80 to 100 kb, and said pair of nucleic acid probes flanking a potential breakpoint in a single chromosome, each of said pair of nucleic acid probes being labeled with at least one different reporter molecule;

hybridizing said pair of nucleic acid probes to the nucleic acid of at least one of said cells; and

detecting the presence of a split signal that arises after a break within said potential breakpoint in the case of a chromosomal aberration.

Please cancel claims 14 and 15 without prejudice or disclaimer.

16. (Previously amended) A diagnostic kit comprising at least the pair of nucleic acid probes of claim 1.

17. (Previously amended three times) The pair of nucleic acid probes of claim 1, wherein the pair of nucleic acid probes hybridize to a single corresponding nucleic acid molecule.

18. (Previously twice amended) The pair of nucleic acid probes of claim 17 wherein the single corresponding nucleic acid molecule is at least a fragment of a chromosome.

19. (Previously twice amended) The pair of nucleic acid probes of claim 18 wherein the chromosome is not aberrant

20. (Previously twice amended) The pair of nucleic acid probes of claim 3 wherein the probes hybridize to a single corresponding nucleic acid molecule.

21. (Previously twice amended) The pair of nucleic acid probes of claim 20 wherein the single corresponding nucleic acid molecule is at least a fragment of a chromosome.

22. (Amended) A method of detecting a break within a potential breakpoint of a single chromosome, said method comprising:

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associating a pair of nucleic acid probes for detection of chromosome aberrations in hematological malignancies and a sample believed to contain nucleic acid complementary to said pair of nucleic acid probes, said pair of nucleic acid probes having comparable size, said size being selected from the group consisting of 1 to 100 kb, 1 to 10 kb, 7 to 15 kb, 10 to 20 kb, 10 to 30 kb, 20 to 40 kb, 30 to 50 kb, 40 to 60 kb, 50 to 70 kb, 60 to 80 kb, 70 to 90 kb and 80 to 100 kb, each nucleic acid probe of said pair of nucleic acid probes being labeled with at least one different reporter molecule and flanking a potential breakpoint in said single chromosome;

hybridizing said pair of nucleic acid probes to said nucleic acid; and

determining whether a split-signal that arises after a break within said potential breakpoint in the case of a chromosomal aberration is present in said sample.

23. (Amended)The pair of nucleic acid probes of claim 22, which pair of nucleic acid probes hybridize to a nucleic acid molecule at a genomic distance of from about 50 kb to no more than 100 kb.

24. (Amended)The pair of nucleic acid probes of claim 22, wherein the at least one reporter molecule of said at least one different report molecule is selected from the group consisting of enzymes, chromophores, fluorochromes, and haptens.

25. (Amended)The pair of nucleic acid probes of claim 24, wherein the pair of nucleic acid probes hybridize to a single corresponding nucleic acid molecule.

26. (Amended)The pair of nucleic acid probes of claim 25, wherein the single corresponding nucleic acid molecule is at least a fragment of a chromosome.

27. (Amended)The pair of nucleic acid probes of claim 26, wherein the chromosome is not aberrant.

28. (Amended)The pair of nucleic acid probes of claim 22 which hybridize *in situ*.

29. (Amended) The pair of nucleic acid probes of claim 28, which pair of nucleic acid probes each hybridize *in situ* to only a few linear DNA molecules per cell.